

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

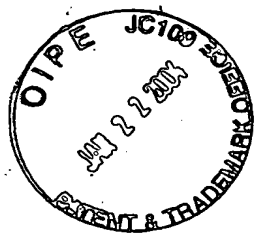
IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**



1 GAATTTGGCC CTCGAGGCCA AGAATTCCGC ACAGGGCGG GCGCCAGCG CAGGCAGAGC GCTGTGCGAT CCGGGCGTC CACCCGCCAT GGGGCTCTCC
CTTAAACCGG GAGCTCCGGT TCTTAAGCCG TGCTCCGGC CGCGGTCTCG CGACAGCGTA GGGCCCGCAG GTGGCGGTA CCCCAGAGG Me tGlyLeuSer
1
101 TGGAGCCCGC GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTCTGT GTGGCTGCCA CTTGGAGCAG GAAACTCCCT TGCCACAGAG AACAGGTTTG
ACCTCGGGC CTGGAGGTGA CGACTACTAG GACGATGACC ACAGAGCAA CACCGACGGT GAACCTCGTC CTTGAGGGA ACGGTGTCTC TTGTCCAAAC
5 TrpSerProA rgProProLe uLeuMetIle uLeuLeuV leuSerLe uTrpLeuPro LeuGlyAlaG lyAsnSerLe uAlaThrGlu AsnArgPheVal
201 TGAACAGCTG TACCCAGGCC AGAAGAAAT GCGAGGCTAA TCCTCGCTTGC AAGGCTGCC TCCAGCACCT GGGCTCTGC ACCTCCAGTT TAAGCAGGCC
ACTGTGCGAC ATGGGTCCGG TCTTTCTTTA CGCTCCGATT AGGCGAACG TTCCGACGGA TGGTCGTGGA CCGAGGACG TGGAGGTCAA ATTCTGTCGG
39 AsnSerCy sThrGlnAla ArgLysLysC ysGluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro
301 GCTGCCCTTA GAGGAGTCTG CCATGTCTGC AGACTGCCTA GAGCAGCAG AACAACTCAG GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGCGCATG
CGACGGGAAT CTCCTCAGAC GGTACAGACG TCTGACGGAT CTCCTGCTGC TTGTTGATC CTTGTGCGA GACTATCTGA CGTCCACGGT AGCCGCGTAC
72 LeuProLeu GluGluSerA laMetSerAl aAspCysLeu GluAlaAlaG luGlnLeuAr gAsnSerSer LeulleAspC ysArgCysHi sArgArgMet
401 AAGCACCAAG CTACCTGTCT GGACATTTAT TGGACCGTTC ACCCTGCCG AAGCCTTGGT GACTACGAGT TGGATGTCTC ACCCTATGAA GACACAGTGA
TTCTGTGTTT GATGGACAGA CCTGTAATA ACCTGGCAAG TGGACCGGC TTCCGAAACCA CTGATGCTCA ACCTACAGAG TGGGATACCT CTGTGTCTACT
105 LysHisGlnA laThrCysLe uAspIleTyr TrpThrValH isProAlaAr gSerLeuGly AspTyrGluL euAspValSe rProTyrGlu AspThrValThr
501 CCAGCAAACC CTGGAATAATG AATCTTAGCA AGTTGAACAT GCTCAAACCA GACTCGGACC TCTGCCTCAA ATTTGCTATG CTGTGTACTC TTCACGACAA
GGTCGTTTGG GACCTTTTAC TTAGAATCGT TCAACTTGTA CGAGTTTGGT CTGAGCCTGG AGACGGAGTT TAAACGATAC GACACATGAG AAGTGTCTGT
139 SerLysPr oTrpLysMet AsnLeuSerL ysLeuAsnMe tLeuLysPro AspSerAspL euCysLeuL ysPheAlaMet LeuCysThrL euHisAspLys
601 GTGTGACCGC CTGCGCAAGG CCTACGGGA GGCATGCTCA GGCATCCGT GCCAGCGCA CCTCTGCCTA GCCCAGCTGC GCTCCTTCTT TGAGAAGGCA
CACACTGGCG GACGCGTTCC GGATGCCCTC CCGTACGAGT CCCTAGGCGA CCGTCGCGT GGAGACGGAT CCGGTGCGACG CGAGGAAGAA ACTCTTCCGT
172 CysAspArg LeuArgLysA laTyrGlyG l ualaCysSer GlyIleArgC ysGlnArgHi sLeuCysLeu AlaGlnLeuA rgSerPhePh eGluLysAla
701 GCAGAGTCCC ACGCTCAGG TCTGCTGCTG TGTCCTGTG CACCAAGA TGCGGGCTGT GGGAGCGGC GGCCTAACAC CATCGCCCC AGTTGCGCCC
CGTCTCAGG TGGAGTCCC AGACGACGAC ACAGGGACAC GTGCTCTTCT ACGCCCGACA CCCCTCGCCG CCGCATTTGT GTAGCGGGG TCAACGCGG
205 AlaGluSerH isAlaGlnG l yLeuLeuLeu CysProCysA laProGluAs pAlaGlyCys GlyGluArgA rgArgAsnTh rIleAlaPro SerCysAlaLeu
801 TGCTTCTGT AACCCCAAT TGCTGGATC TGCGGAGCTT TGCGGAGCTT GACCTTTGT GCAGATCAG CCTGATGGAC TTCCAGACCC ACTGTCTATCC
ACGAAGACA TTGGGGTTA ACGGACCTAG ACGCTCGAA GACGGACGC CTGGAAACA CGTCTAGTGC GGACTACCTG AAGTCTGGG TGACAGTAGG
239 ProSerVa lThrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC ysArgSerAr gLeuMetAsp PheGlnThrH isCysHisPro
901 TATGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGCTGCGGG CATACCTGGG GCTGATTGGG ACTGCCATGA CCCCAACTT CATCAGCAAG
ATACCTGTAG GAACCTGAA CACGTTGACT CGTCAGGTCT ACAGACGCCC GTATGGACCC CGACTAACCC TGACGGTACT GGGGTTTGA GTAGTCGTTT
272 MetAspIle LeuGlyThrC ysAlaThrG l uGlnSerArg CysLeuArgA laTyrLeuG l yLeuIleGly ThrAlaMetT hrProAsnPh eIleSerLys

FIG. 1A



1001 GTCAACACTA CTGTTGCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGTCTCCCAG AACCCCTGCC
CAGTTGTGAT GACAACGGAA TTTCGACGTGG ACGGCTCCGT CGCCGTTGGA TGCTCTGCTC ACACCTGTGC ACCTTTCCAG GAAGAGGGTC TTGGGGACGG
305 ValAsnThr hrValalaLe uSerCysThr CysArgGlyS erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu
1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
AGCACTCCG GTAACGTCGA TTCTACGCCA AGGTGCTGT GTACAGAGAGG GTCCTGACCC GTCTGAGATG AAAAGTCAC CACGTCGTGC TCTTGTCTGT
339 ValGluAl aIleAlaala LysMetArgP heHisArgG1 nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG InAsnSerAsn
1201 CCCTGCTCTG AGACTGCAGC CCAGGCTACC CATCTTTCT TTCTCCATCC TTCCCTTGAT TCTGCTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGAACTA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
372 ProAlaLeu ArgLeuGlnP roArgLeuPr oIleLeuSer pheSerIleL euProLeuI ThrLeuTrp
1301 CTTTGTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCA GCTGTGGAA GAAGACGGAG CGTGTACAC AGCAACCCGG
GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCTCT CTGAGCGGT CGGACACCTT CTTCTGCGTC GCAGATGTG TCGTTGGGCC
1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAAC
TTGGTTGGTC CGTAAGCGCT CGTGTAGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTGG
1501 TCCCTTGCCC CTGCTTCCCT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTTCTGATG GTGATTAGCG GCTCACCTCC
AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
1601 AGCGCTTCTT CCTGTTTCCC AGGACCACC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGTGACTG
TCGGAAGAA GGACAAAGG TCCTGGTGGG TCTCCGATT CTTAGTCACT AAGGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAAGA CTCCACTGAC
1701 AGAAAAATGT TTCTTTTGTG TGAAGGCTG GTGCTCCAGC CTCCACGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
TCTTTTITACA AAGGAACAC ACCTTCCGAC CACGAGGTGCG GAGGTGCAGG GAGACTTACC TTCTATTTTTT GGACGACCAC AGAAGTACG AGACGGTCCG
1801 AATCTGAAC ATTGTTGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC TGTCCTCCAAA TTCCCTCTAGT CCCTTGGGTC ATGATTAAAC
TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAAT GAGGATAATG ACAGGGGTTT AAGGGATCA GGAACCCAG TACTAATTG
1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA
TAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTTT

FIG. 1B

rGFRa1	1	MFLATLYFALP	LLD	LLMSAEV	SGG	DR	LCVKA	ASD	QQ	CL	KE	QS	CS	TK	YRT
rGFRa2	1	MILANAFCL	FFFL	DET	LRSLASR	SS	LQ	SEL	HGW	R	PQ	VD	CV	RA	AN	EL
mGFRa3	1	MGLSWS	PRPPL	L	M	ELL	VL	SL	WPL	PLG	AG	NS	L	AT	EN	RF
																VNS
																CT
																QAR
																KKCE
																AN
																PA
																CKA
																AYQH
rGFRa1	49	LRQ	CV	AG	KE	TN	SS	TS	G	LE	A	K	D	E	CR	S
rGFRa2	60	LRQ	CL	A	G	R	D	R	NT	ML	A	N	K	E	C
mGFRa3	61	L	G	S	C	T	S	S	L	S	R	P	L	P	LE
																ES
																AM
																S
																AD
																CE
																AD
																CL
																D
																I
																Y
																W
																S
																M
																Y
																Q
																Y
																M
																Y
																W
																H
																P
																HP
																AT
																CL
																D
																I
																Y
																W
																S
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y
																M
																Y
																Q
																Y

hGFra3 1 MVRPLNPRPLPPVVLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRK
mGFra3 1 . . MGLSWSPPPLLLMILLVLSLW.LPLGAGNSLATENRFVNSCTQARKK

hGFra3 51 CQADPTCSAAYHHLDSCTSSIISTPLPSEEPSVPAADCLEAAQQLRNSSLIG
mGFra3 48 CEANPACKAAYQHLGSCSTSSLSRPLPLEESAMSAADCLEAAEQQLRNSSLID

hGFra3 101 CMCHRRMKNQVACLDIYWTVHRAARSLGN YELDVSPYEDTTSKPKWKMNLS
mGFra3 98 CRCHRRMKHQATCLDIYWTVHPARSLGD YELDVSPYEDTTSKPKWKMNLS

hGFra3 151 KLNMLKPDSDLCLKFAMLC TLN DKCDRLRKAYGEACSGPHCQRHVCLRQL
mGFra3 148 KLNMLKPDSDLCLKFAMLC TLH DKCDRLRKAYGEACSGIRCQRHLC LAQL

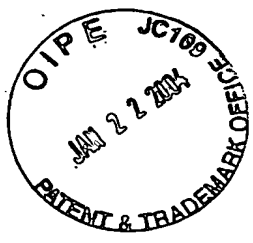
hGFra3 201 LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
mGFra3 198 RSFFEKAAESHAQGLLLCPCAPE DAGCGERRRNTIAPSCALP SVTPNCLD

hGFra3 251 LRLCFSDPLCRSRLVDFQTHCHPMDILGTCA TEQSRCLRAYLGLIGTAM
mGFra3 248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCA TEQSRCLRAYLGLIGTAM

hGFra3 301 TPNFVSNVNTSVALSCTCRGSGNLECEMLEGFFSHNPCLTEAIAAKMR
mGFra3 298 TPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMR

hGFra3 351 FHSQLFSQDWPHPPTFAVMAHQENPAVRPQPWVPSLFSCTLP LILLLSLW
mGFra3 348 FHRQLFSQDWA DSTFSV VQQQNSNPA LRLQPRLPILSFSI LP LILLQLTLW

FIG. 3



48613	1	MVRPLNPRPLPPVVLMLLLPLPPSPLPLAAGDPLPTESRLMNSCLQARRK
48614	1	MVRPLNPRPLPPVVLMLLLPLPPSPLPLAAGDPLPTESRLMNSCLQARRK
48613	51	CQADPTCSAAYYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614	51	CQADPTCSAAYYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48613	101	CMCHRRMKNQVACLDIYWTVHRRARSLGNYELDVSPYEDTVTSKPWKMNLS
48614	101	CMCHRRMKNQVACLDIYWTVHRRARSL.....
48613	151	KLNMLKPPDSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614	127DSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48613	201	LTFFFEKAAEPPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614	170	LTFFFEKAAEPPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48613	251	LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48614	220	LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48613	301	TPNFVSNVNTSVALSCTCRSGGNLQEECEMLEGFFFSHNPCLTEAIAAKMR
48614	270	TPNFVSNVNTSVALSCTCRSGGNLQEECEMLEGFFFSHNPCLTEAIAAKMR
48613	351	FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLSLW
48614	320	FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLSLW

FIG. 4

DNA48613.orf 1 A T G G T G C G C C C C C C T G A A C C C G C G A C C G C T G C C G C C C G T A G T C C T G A T G T T
GENFRal.orf 1 A T G A T C T T G G C A A A C G T C T T C T G C C T C T I C T I C T I T C T
GENFRa2.orf 1 A T G A T C T T G G C A A A C G T C T T C T G C C T C C T C C C T G C A G G G C C C C G

DNA48613.orf 51 G C T G C T G C T G C C C C C G T C G C C C C T G C C C T C T C G C A G C C C G A G A C C C C C
GENFRal.orf 6 C C T G G C G A C C C T G T A C T T C G C G C T G C C G C T T G G A C T T G C T C C T G T C G G
GENFRa2.orf 39 A G A C G A G A C C C T C C G C T C T T G G C C A G C C C C C A G T G G A C T G C A G G G C C C C G

DNA48613.orf 101 T T C C C A C A G A A G C C G A C T C A T G A A C A G C T G T C T C C A G G C C A G G A G A A G
GENFRal.orf 56 C C G A A G T A G C G G C G G A G A C C G C C T G G A T T G C G T G A A A G C C A G T G A T C A G
GENFRa2.orf 89 A G C T C C A C G G C T G G C G C C C C A G T G G A C T G T G T C C G G C C A A T G A G C T G

DNA48613.orf 151 T G C C A G G C T G A T C C C A C C T G C A G T G C T G C C T A C C A C A C C T G G A T T C C T G
GENFRal.orf 106 T G C C T G A A G A G C A G A G C T G C A G C A C A G T A C C G C A C G C T A A G G C A G T G
GENFRa2.orf 139 T G T G C C G C C G A A T C C A A C T G C A G C T C T G C T A C C G C A C T C T G C G G C A G T G

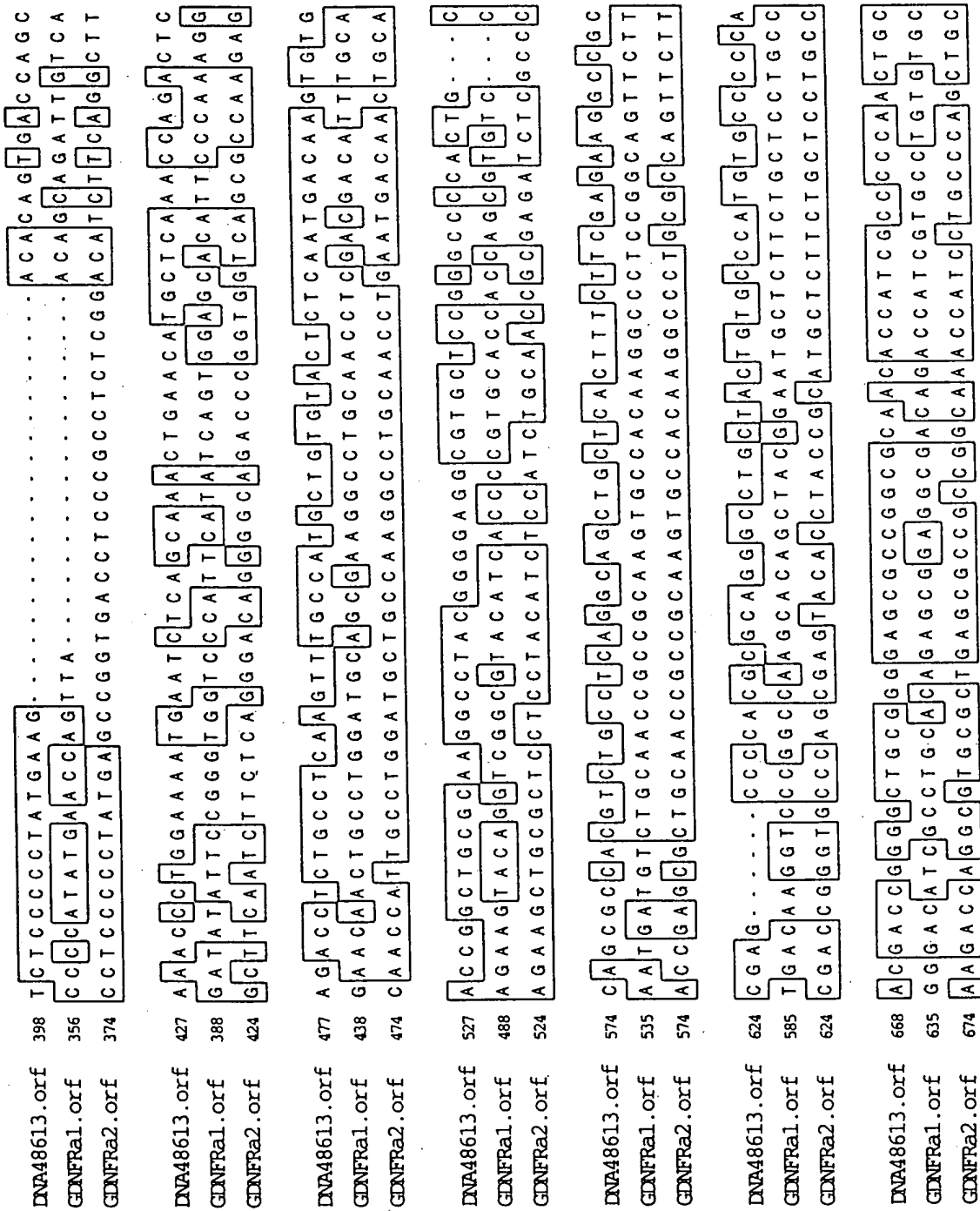
DNA48613.orf 201 C A C C T C T A G C A T A A G C A C C C C A C T G C C C T . . . C A G A G A G C C T T C G G T C C
GENFRal.orf 156 C G T G G C G G G C A A G A G A C C A A C T T C A G C C T G G C A T C C G G C C T G G A G G C C A
GENFRa2.orf 189 C C T G G C A G G C C G C G A C C G C A A C C A T G C T G G C C A

DNA48613.orf 248 C T G C T G A C T G C C T G G A G G C A G C A C A C T C A G G A C A G C T C T G A T A
GENFRal.orf 206 A G G A T G A T G C C G C A G C G C C A T G G A G G C C C T G A A G C A G A G T C G C T C T A C
GENFRa2.orf 224 A C A A G G A G T G C C A G G C G G C C T T G G A G G T C T T G C A G A G A G C C C G C T G T A C

DNA48613.orf 298 G G C T G C A T G T G C C A C C G G C G C A T G A A G A A C C A G G T T G C C T G C T T G G A C A T
GENFRal.orf 256 A A C T G C C G C T G C A A G C G G G T A T G A A G A A G G A G A A G A C T G C C T G C G C A T
GENFRa2.orf 274 G A C T G C C G C T G C A A G C G G G C A T G A A G A A G G A G C T G C A G T G T C T G C A G A T

DNA48613.orf 348 C T A T T G G A C C G T T C A C C G T G C C C G C A G C C T T G G T A A C T A T G A G C T G G A T G
GENFRal.orf 306 T T A C T G G A G C A T G T A C C A G A G C C T G C A G G A A T G A T C T G C T G G A G G A T T
GENFRa2.orf 324 C T A C T G G A G C A T C A C C T G G G G C T G A C C G A G G T G A G G A G T T C T A C G A A G

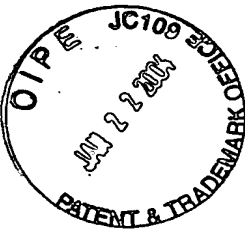
FIG. 5A



மேல்

DNA48613.orf	718	G	C	G	C	T	G	C	C	...	G	C	C	T	G	T	G	C	C	C	C	C	A	A	C	T	G	C	C	T	G	G	A	G	C	T	G	C	G	C	T	C	T	G																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
GINFral1.orf	685	T	C	C	T	A	T	G	A	A	G	A	G	A	A	G	C	C	C	A	A	C	T	G	T	T	G	A	A	T	T	G	C	A	G	G	A	C	T	C	C	T	G																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
GINFral2.orf	724	T	C	C	T	A	T	G	A	G	A	C	A	A	G	A	A	G	C	C	C	A	A	C	T	G	C	C	T	G	G	A	C	T	G	C	T	G	C	G	T	G	C	T	G																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
DNA48613.orf	765	C	T	T	C	T	C	G	A	C	C	C	G	C	T	T	T	G	C	A	G	A	T	C	A	G	C	C	T	G	G	A	T	T	C	C	A	G	A	C	C	A	C	T																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
GINFral1.orf	735	C	A	A	G	A	C	G	A	A	T	T	A	C	A	T	C	T	G	C	A	G	A	T	C	T	G	C	C	T	G	C	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T

FIG. 5C



DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
GINFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C C T T C C C A G T A C A G A C C A C C A C T G
GINFRa2.orf 1074 C A C G A C G T G A A C G T G T C C C C A A A G G C C C C T C G T T C C A G G C C A C C C A G G

DNA48613.orf 1103 T G G C A C A C A G A T G A A A C C C T G C T G T G A G G C C A C A G C C C T G G T G C C C
GINFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C G G G T T A A G A A C A A A C C C C T G G G C C A G C A
GINFRa2.orf 1124 C C C C T C G G G T G G A G A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

DNA48613.orf 1153 T C T C T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
GINFRa1.orf 1129 G G G T C T G A G A A T G A A T T C C C A C T C A T G T T T G C C A C C G T G T G C A A A T T T
GINFRa2.orf 1174 A C C A G C T T G G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

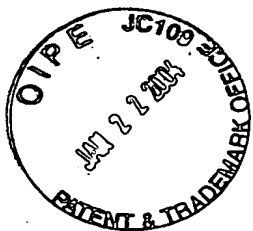
DNA48613.orf 1203 G
GINFRa1.orf 1179 A C A G G C A C A G A A G C T G A A T C C A A T G T G T C G G G C A A T A C A C A C A C T C T G T A
GINFRa2.orf 1224 G G G G C T G A A G G C C A C A A C T C C A A A G A G T A A G C A T G T G C T T C A C A G A G C

GINFRa1.orf 1229 T T T C C A A T G G T A A T T A T G A A A A G A A G G T C T C G T G C T T C C A G C C A C A T A
GINFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G T G A T C A A A C C T A A C T C A

GINFRa1.orf 1279 A C C A C A A A A T C A A T G G C T G C T C C A A G C T G T G G T C T G A G C C C A C T G C T
GINFRa2.orf 1324 G G C C C C A G C A G A G C C A G A C G T C G G C T G C C T T G A C C G T G C T G T C T G T C C T

GINFRa1.orf 1329 G G T C C T G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T A A C A G A A A C A T
GINFRa2.orf 1374 G A T G C T G A A A C A G G C C T T G T A G
GINFRa1.orf 1379 C A T A G

FIG. 5D



DNA48613 1 MVRPLNPRPLPPVVLMLLLLLPSPPLPLAAGDPLPTESRLMNSCLQARRK
GDNFra1 1 MFLAT--LYFALL--PLLDLLLSA--EVSGGD--RL--DCVKASDQ
GDNFra2 1 MILANVFCLFFFLDET LRS LASPS--SLQGPELHGWRPPV--DCVRANEL

DNA48613 51 CQADPTCSAAYHHLDSC TSSISTPLP·SEEPSVPADCLEAAQQLRNSSLI
GDNFra1 36 CLKEQSCSTKYRTL RQCVAGKETN FSLASGLEAKDECRSAMEALKQKSLY
GDNFra2 47 CAAESNCSSRYRTL RQCLAGRD RN--TMLANK ECAALEVLQESPLY

DNA48613 100 GCMCHRRRMKNQVA CLDIYWTVHRARSLGNYELDVSPYEOTVTSKPWKMN L
GDNFra1 86 NCRCKRGMKKEKNCLRIYWSMYQSL·QGNOLL EDSPYEPVNSRLSDIFRV
GDNFra2 92 DCRCKRGMKKELOCLQIYWSIHLGLTEGE E FYEASPYEPVTSRLSDIFRL

DNA48613 150 SKL--NMLKPOS DLCLKFAMLCTLNDKCDRLRKAYGEACS--
GDNFra1 135 VPFIS--VEHI--PKGN NCLDAAKACNLDDICKKYRSAYITPCTTSVS·
GDNFra2 142 ASIFS GTGADPVVSAKSNHCLDAAKACNLNDNCKKLRS SYISICNREIS P

DNA48613 188 GPHCORHVC L RQLLTFFEKAAEPHAQGLLLCP CAPNDRGCGERRRNTIAP
GDNFra1 179 NDVCNRRKCHKALRQFFDKVPAKHSGYMLFCSC--RDI ACTERRRQTIVP
GDNFra2 192 TERCNRRKCHKALRQFFDRVPSEYTYRMLFCSC--QDQACAERRRQTILP

DNA48613 238 NCALPPVA·PNCLELRRLCFSDPLCRSRLVDFQTHCHP·MDILGT CATEQ
GDNFra1 227 VCSYEEREKPNCLNLQDSCKTNYICRSRLADFFTNCOPESSRSVSSCLKEN
GDNFra2 240 SCSYEDKEKPNCLDLRGVCR TDHLCRSRLADFHANCRASYQTVTSCPADN

DNA48613 286 ·SRCLRAYLGLIGTAMTPNFVSNV·NTSVALSCTCRGSGN LQEECEMLE
GDNFra1 277 YADCLLAYSGLIGTVMTPNYIDSS·SLSVAPWCD CSNSGNDLEECLKFL
GDNFra2 290 YQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCS CRGSGNMEECECKFL

DNA48613 333 GFFSHNPCLTEAIAA·KMRFHSQLFS
GDNFra1 325 NFFKDN T CLKNAIQAFNGS DVTVWQPAFPVQT TATT T TALRVKNKPLG
GDNFra2 340 R DFTENPCLRNAIQAFNGT DVNVSPKGPSFQATQAPRVEKTPSLPDDL S

DNA48613 358 Q·DWPHPPTFAVMAHONENPAVRPQ·
GDNFra1 375 PAGSENEIPTHVLP PCANLQAQKLKSNVSGNTHLCISNGNYEKEGLGASS
GDNFra2 390 OSTSL--LGTSVIT TCTSVQEQGLKANNSKELSM CFT·ELTTNIIPGSN

DNA48613 381 ·PWVPSLFSCTLP L I L L L S L W·
GDNFra1 425 HITTKSMAAPP SCGLSPLLVLVVTALSTLLSLTETS
GDNFra2 435 KVIK P NSGPSRARPSAALT VLSVLM LKQAL·

FIG. 6

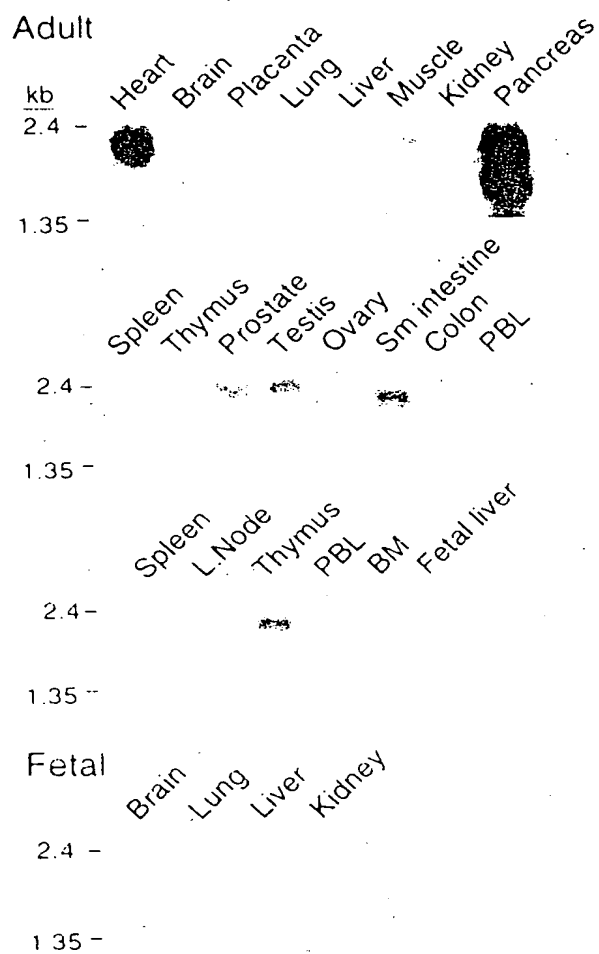


FIG. 7

GFR α 3

GFR α 2

GFR α 1

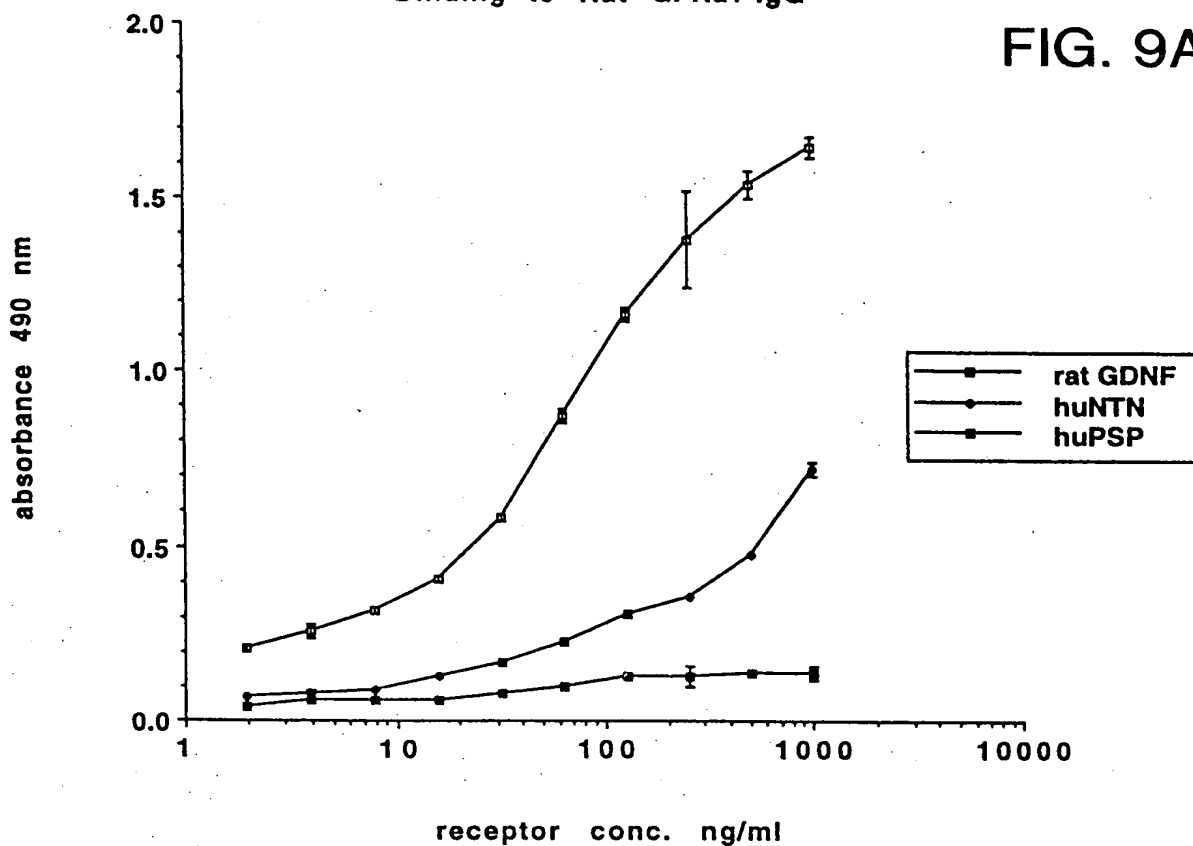


FIG. 8



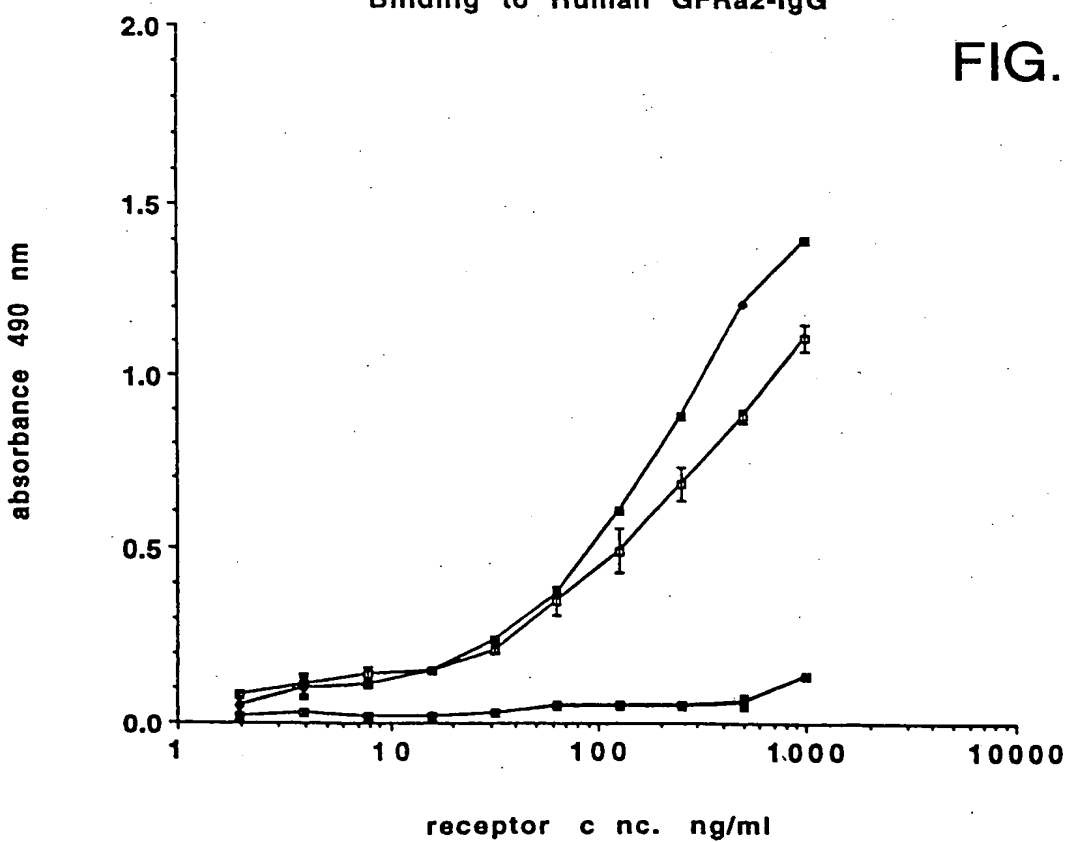
Binding to Rat GFRa1-IgG

FIG. 9A

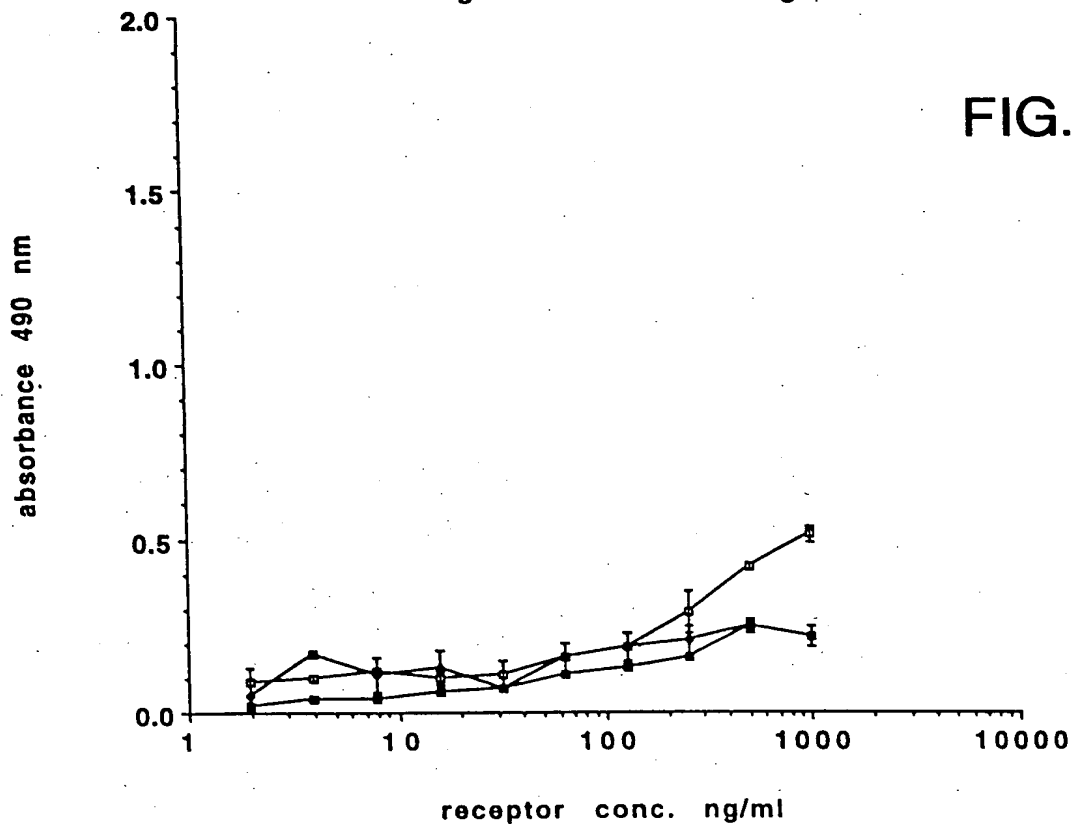


Binding to Human GFRa2-IgG

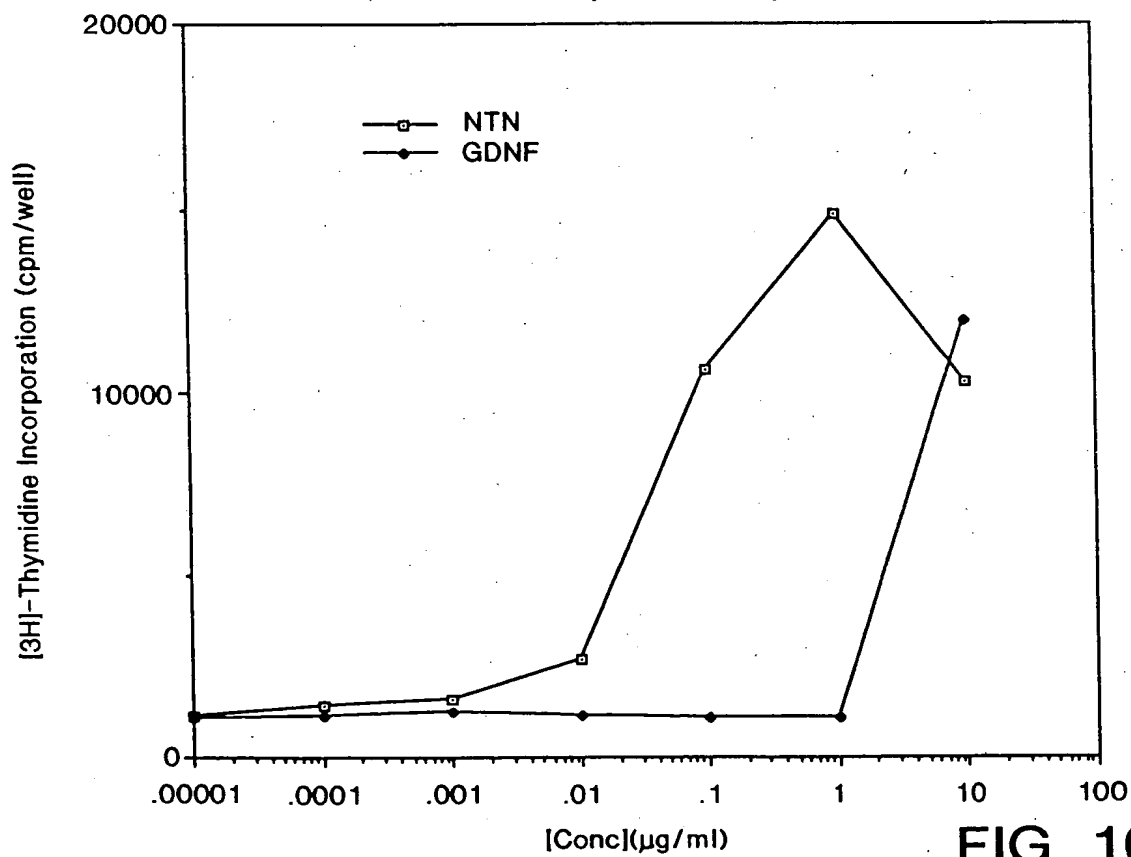
FIG. 9B



Binding to Human GFRa3-IgG



Proliferation of Ba/F3-GFRa2-mpl cells in response to NTN and GDNF



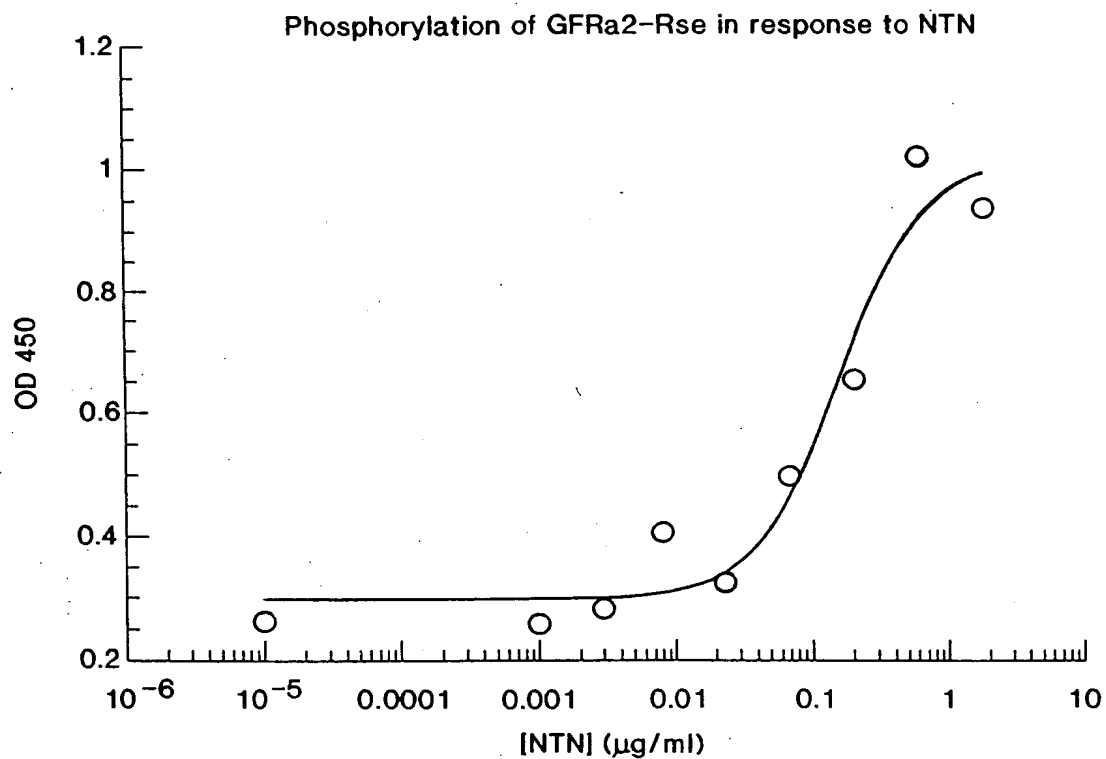
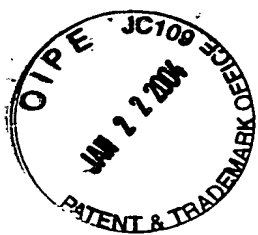


FIG. 11

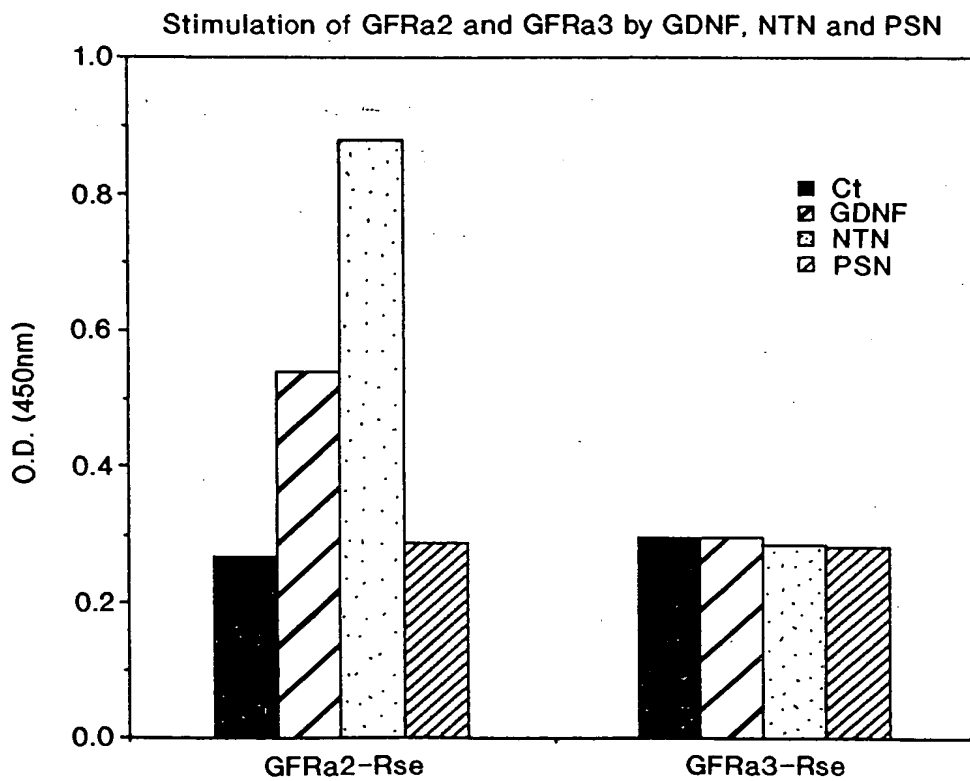


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

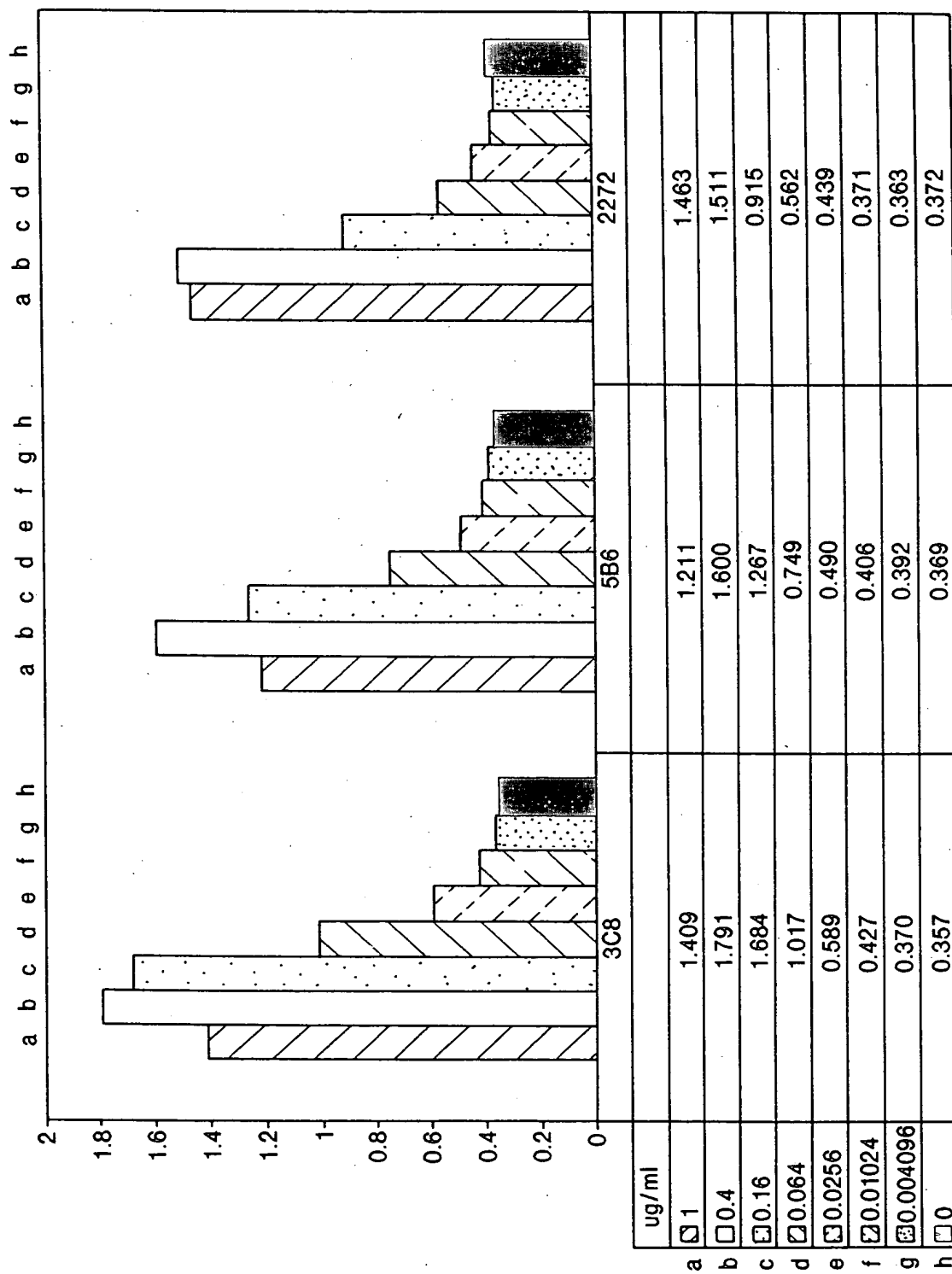


FIG. 13